Systematic analysis of gene expression alterations and clinical outcomes of adenylate cyclase-associated protein in cancer

Supplementary Materials



Supplementary Figure 1: CAP1 gene analysis in Head-Neck and lung cancer (Oncomine database). The box plot comparing specific CAP1 expression in normal (left plot) and cancer tissue (right plot) was derived from Oncomine database. The analysis was shown in Head-Neck carcinoma relative to normal Head-Neck (A), in lung carcinoma relative to normal lung (**B**).



Supplementary Figure 2: CAP1 gene analysis in Leukemia cancer (Oncomine database). The box plot comparing specific CAP1 expression in normal (left plot) and cancer tissue (right plot) was derived from Oncomine database. The analysis was shown in leukemia carcinoma relative to normal tissue.



Supplementary Figure 3: CAP1 gene analysis in Lymphoma, Melanoma and Bladder cancer (Oncomine database). The box plot comparing specific CAP1 expression in normal (left plot) and cancer tissue (right plot) was derived from Oncomine database. The analysis was shown in Lymphoma carcinoma relative to normal tissue (A), in Melanoma relative to normal tissue (B). in Bladder cancer relative to normal bladder (C).



Supplementary Figure 4: CAP1 genes in Breast, Ovarian, Gastric and Lung cancer (Kaplan-Meier Plotter). The survival curve comparing the patient with high (red) and low (black) expression in breast, ovarian, gastric and lung cancer was plotted from Kaplan-Meier plotter database.



Supplementary Figure 5: CAP2 gene analysis in Leukemia, Gastric, Breast and Renal cancer (Oncomine database). The box plot comparing specific CAP2 expression in normal (left plot) and cancer tissue (right plot) was derived from Oncomine database. The analysis was shown in Leukemia relative to normal (A), in gastric carcinoma relative to normal gastric (B), in in breast carcinoma relative to normal breast (C), in renal carcinoma relative to normal renal (D).



Supplementary Figure 6: CAP2 gene analysis in Bladder and Renal cancer (Oncomine database). The box plot comparing specific CAP2 expression in normal (left plot) and cancer tissue (right plot) was derived from Oncomine database. The analysis was shown in Bladder relative to normal bladder (A), in Glioblastoma relative to normal tissue (B).



Supplementary Figure 7: CAP2 gene analysis in Ovarian, Colon, Lung, Esophagus, Prostate and Melanoma cancer (Oncomine database). The box plot comparing specific CAP2 expression in normal (left plot) and cancer tissue (right plot) was derived from Oncomine database. The analysis was shown in Ovarian relative to normal ovarian (A), in Colorectal relative to normal tissue (B), in Lung cancer relative to normal ovarian (C), in Esophagus relative to normal tissue (D), in Prostate cancer relative to normal prostate (E), in Melanoma relative to normal tissue (F).



Supplementary Figure 8: CAP2 genes in Brain, Prostate and Blood cancer (PrognoScan database). The survival curve comparing the patient with high (red) and low (black) expression in brain, prostate and blood cancer were plotted from PrognoScan database as the threshold of cox *p*-value < 0.05.



Supplementary Figure 9: The example shows that genes that alter CAP1, CAP2 in Prostate have a tendency toward co-occurrence. The *P* values are determined by a Fisher's exact test, P < 0.05 (A). A plot showing the relationship between CAP1, CAP2 mRNA abundance and CNA in the CAP1, CAP2 gene in tumors from the selected cancer study (**B**, **C**). The "x"s indicate individual tumors, and the circles indicate tumors with missense mutations. Homdel, homozygously deleted; Hetloss, heterozygously deleted; Diploid, two alleles present; Gain, low-level gene amplification event; Amp, high-level gene amplification event; Mutated, nonsynonymous mutation; Normal, no mutation or CNA present.



Estilo, Head-Neck

Supplementary Figure 10: CAP1 genes in Head-Neck cancer. CAP1 is coexpressed with the indicated 52 genes across a panel of 32 Head-Neck and 26 normal Head-Neck samples. Bar length represented the significance and negative logarithm of enrichment *p*-value.



Supplementary Figure 11: CAP2 genes in Brain, Prostate, Bladder and Lung cancer. CAP2 is coexpressed with the indicated 513 genes across a panel of 157 Brain and 23 normal Brain samples, 521 genes across a panel of 89 Prostate and 23 normal prostate samples, 1051 genes across a panel of 109 Bladder and 48 normal bladder samples, 35 genes across a panel of 65 Lung and 28 normal lung samples. Bar length represented the significance and negative logarithm of enrichment *p*-value.



Supplementary Figure 12: The potential pathway and GO processes were visualized by ICGC Data Portal with CAP1(A) and CAP2 (B).

Cancer Subset	In	Nearest Peak	#Genes In Peak	Ormalian	Frequency of Ampl		lification	in the second	In	and the second se	Genes	-	Frequency of Delet		
	Peak?			4.000	Overall	Focal	High-level	Cancer subset	Peak?	Nearest Peak	in Peak	4-14-14	Overall	Focal	H
L_cancers	No	chr1:29915914-40225249	7	1.298-11	0.1709	0.0613	0.0147	all_cancers	No	chr1:26397970-27516104	24	1.0	0.1185	0.0147	0.0
ing NSC	Yes	chr1:39594268-40694964	30	5.038-6	0.2524	0.0887	0.0232	Myeloproliferative disorder	Yes	chr1:742429-45006976	585	0.0255	0.0279	0.0279	0
karian	Yes	chr1:39297788-43447561	52	0.00167	0.2524	0.1942	0.0291	Medulioblasterna	Yes	chr1:742429-58517991	700	0.773	0.0703	0.0156	0
il.hematologic	Yes	Chr1:36669764-47094569	346	0.0501	0.03	0.0086	0.0043	Esophageal squamous	Yes	Chr1:742429-41746845	538	1.0	0.1591	0.0227	0
dute lymphoblastic leukemia	Yes	01135626744-47094569	166	0.074	0.0153	0.0128	0.0051	Lung SC	Yes	chr1:742429-247135059	1967	1.0	0.2	0.0	0
Intel	Yes	Chr1:32459181-68120069	333	0.311	0.2305	0.1317	0.0329	Qvecieo	Yes	chr1:19832656-117038289	761	1.0	0.1165	0.0194	0
il cothelal	No	chr1:39927775-40235249		1.745-13	0.22	0.087	0.0212	Enostate	Yes	chr1:742429-201213710	1639	1.0	0.1304	0.0435	
il. luca	No	Chr1:39927775-40164339	\$	9.265-13	0.27	0.1021	0.0323	Hepatocellular	No	chr1:53737764-06641362	141	0.635	0.157	0.0248	4
una SC	No	chr1:40092174-40164329	1	1.652-8	0.575	0.325	0.2	Acute hymphoblestic loukemia	No	chr1:47429728-47652865	5	1.0	0.0281	0.0	
acchaosal souemous	No	chr1:118282114-118007006	2	1.0	0.3409	0.0682	0.0	Breast	No	chr1:7843010-34898808	348	1.0	0.2263	0.0288	
fiveloproliferative disorder	No	No peak on chromosome	0	1.0	0.014	0.0	0.0	Colorectal	No	chr1:3756301-31327853	325	1.0	0.1366	0.0124	
iltextal	No	chr1:97553627-143814998	166	1.0	0.1106	0.0184	0.0045	Glioma	No	chr1:3802708-6239708	11	1.0	0.122	0.0	
loiscectal	No	UN11143657867-170995569	459	1.0	0.1366	0.0373	0.0062	Lune NSC	No	chr1:6627943-33011301	340	1.0	0.131	0.0109	
Ziona	No	chr1:202625619-202824653	3	1.0	0.2683	0.0488	0.0	Melanoma	No	chr1+68718027-143600822	281	1.0	0.2252	0.018	
lepstocellular	No	chr11145279761-156420150	265	1.0	0.0579	0.0083	0.0	Benal	No	chr1:742429-29081584	390	1.0	0.1111	0.0	-8
And a look a store a	No	No peak on chromosome	0	1.0	0.0859	0.0078	0.0	all epithelial	No	chr1:26771712-27516104	13	1.0	0.1517	0.016	
Idanoma	No	chr1:120041950-120160448	1	1.0	0.2523	0.018	0.0	all hematologic	No	chr1.47410726.47652865		10	0.03	6.01	
rostate	No	chr1:143798352-207231108	682	1.0	0.087	0.0326	0.0	all second	No	chr1/34454731-38347234	+05	10	0 1100	0.0292	10
anal	Res.	chr1:143368034-109251103	100	1.0	0.1667	0.0397	0.0	PELONDE		NILARSSON AND AND AND	100		0.1170	0.0074	
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E cancers reast varian	Yes Yes Yes	dy6:110391-23626250 chr6:8663316-22771501 chr6:4559991-22453081	95 50 93	1.0 0.0333 0.0386	0.2162 0.3333 0.301	0.0051 0.1358 0.1553	High-level 0.0166 0.0535 0.068	all cancers all hemitologic Surra.NSC	Peak? No Yos Yes	ct=6:15536:30-2553994 ct=6:110391-20509888 ct=6:110391-20509888	2 90 90	Questue 5.0 0.0466 5.0	Overall 0.1115 0.0272 0.1282	Focal 0.024 0.0172 0.0232	
L.concers stant saciant L.conthelial	Yes Yes Yes	cm6.110391-23626260 cm6.8665316-22771501 cm6.459991-22453001 cm6.110291-24080365	95 50 93 95	1.0 0.0333 0.0386 0.699	Overall 0.2162 0.3333 0.301 0.2016	Fecal 0.0351 0.1358 0.1553 0.0492	High-level 0.0166 0.0535 0.068 0.0217	el cencera al hermatologic Luna NSC Ovacian	Peak? No Yos Yos Yos	ctri611553630-2552994 ctri61150591-20559888 ctri61120591-20559888 ctri61120591-1052998902 ctri61112051-105299492	in Peak 2 90 90 939	Qualue 1.0 0.0466 1.0 1.0	Overall 0.1115 0.0272 0.1282 0.068	Fecal 0.024 0.0172 0.0232 0.0097	
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Supplementary Figure 13: Examples of Tumorscape data analysis and visualization. (A–B) shows that CAP1 was most frequently amplified and deletion in lung, ovarian, breast, prostate, leukemia cancer; (C–D) shows that CAP2 was most frequently amplified and deletion in lung, ovarian, prostate, breast cancer; The q-value represents the likelihood of a random occurrence of the specific amplification/deletion that is calculated based on the background copy number variation. The table depicts a list of cancers in which the representative gene (*CAP1, CAP2*) is located in or near the frequently amplified region (orange and yellow rows, respectively).